# RAW SEQUENCE LISTING

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Application Serial Number: 10/561,015
Source: IFWP
Date Processed by STIC: 12/30/2005

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IFWP

**RAW SEQUENCE LISTING** DATE: 12/30/2005
PATENT APPLICATION: **US/10/561,015** TIME: 09:36:55

Input Set : **A:\Sequence Listing PCTUS04019934.txt**
Output Set: **N:\CRF4\12302005\J561015.raw**

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  3 <110> APPLICANT: Felsenfeld, Dan P.
  4       Verse-Pierluissi, Maria A.
  6 <120> TITLE OF INVENTION: METHODS AND AGENTS FOR TREATING AXONAL DAMAGE, INHIBITION OF
  7       NEUROTRANSMITTER RELEASE AND PAIN TRANSMISSION, AND BLOCKING
  8       CALCIUM INFLUX IN NEURONS
 10 <130> FILE REFERENCE: 02420/100M761-US1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/561,015
C--> 12 <141> CURRENT FILING DATE: 2005-12-16
 12 <150> PRIOR APPLICATION NUMBER: 60/480,092
 13 <151> PRIOR FILING DATE: 2003-06-19
 15 <150> PRIOR APPLICATION NUMBER: PCT/US04/19934
 16 <151> PRIOR FILING DATE: 2004-06-21
 18 <160> NUMBER OF SEQ ID NOS: 27
 20 <170> SOFTWARE: PatentIn version 3.3
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 24 <212> TYPE: PRT
 25 <213> ORGANISM: Artificial sequence
 27 <220> FEATURE:
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 53 <213> ORGANISM: artificial sequence
 55 <220> FEATURE:
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 64 Gln Phe Asn Glu Asp Gly Ser Phe Ile Gly Gln Phe
 65             20                  25
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166 ccaccctgag gcattacatc tggagtgcca gtcggacact agcctgctac tgcactggca   2820
168 gccaccactc agccacaatg gagtgctcac tggctacctg ctctcttacc atcccttgga   2880
170 tggggaaagc aaagagcagt tgttcttcaa cctttcggac ccagagctcc ggactcataa   2940
172 tctcaccaac ctcaaccctg atctacagta ccgcttccag cttcaggcca ccacccaaca   3000
174 gggtcctggt gaggccattg tgcgtgaagg aggcactatg gccctatttg gcaagccaga   3060
176 ttttggcaac atttcagtca cagcaggtga aaactacagt gtggtctcct gggtccctcg   3120
178 ggagggccag tgcaatttca ggttccacat cctgttcaaa gccttgccag aagggaaagt   3180
180 gagccctgat caccagcctc agcctcaata tgtgagctac aatcagagct cctacacaca   3240
182 gtgggaccta cagcctgaca ccaaatatga gatccacctg atgagggaga aggtcctctt   3300
184 gcaccatctg gctgtgaaga ctaatggcac tggccccgtg cgagtgtcga ctaccggtag   3360
186 ctttgcctcc gagggctggt tcatcgcctt tgtcagtgct atcattctct tgctcctcat   3420
188 cctgctcatc ctctgcttca tcaaacgcag caagggcggc aaatattcag tgaaggacaa   3480
190 ggaggacact caggtagatt ccgaggcccg gcccatgaaa gacgagacct tcggcgagta   3540
192 caggtccctg gagagtgaca atgaagagaa ggccttcggc agcagccagc catctctcaa   3600
194 tggagacatc aaacccctag gcagtgatga cagtctggct gattatgggg gcagtgtgga   3660
196 tgtccagttc aatgaggatg gctctttcat cggccaatac agtggcaaaa aagagaagga   3720
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204 <211> LENGTH: 1259
205 <212> TYPE: PRT
206 <213> ORGANISM: Rattus rattus
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215             20                  25                  30
218 Glu Pro Pro Val Ile Thr Glu Gln Ser Pro Arg Arg Leu Val Val Phe
219         35                  40                  45
222 Pro Thr Asp Asp Ile Ser Leu Lys Cys Glu Ala Arg Gly Arg Pro Gln
223     50                  55                  60
226 Val Glu Phe Arg Trp Thr Lys Asp Gly Ile His Phe Lys Pro Lys Glu
227 65                  70                  75                  80
230 Glu Leu Gly Val Val Val His Glu Ala Pro Tyr Ser Gly Ser Phe Thr
231                 85                  90                  95
234 Ile Glu Gly Asn Asn Ser Phe Ala Gln Arg Phe Gln Gly Ile Tyr Arg
235             100                 105                 110
238 Cys Tyr Ala Ser Asn Asn Leu Gly Thr Ala Met Ser His Glu Ile Gln
239         115                 120                 125
242 Leu Val Ala Glu Gly Ala Pro Lys Trp Pro Lys Glu Thr Val Lys Pro
243     130                 135                 140
246 Val Glu Val Glu Glu Gly Glu Ser Val Val Leu Pro Cys Asn Pro Pro
247 145                 150                 155                 160
250 Pro Ser Ala Ala Pro Leu Arg Ile Tyr Trp Met Asn Ser Lys Ile Leu
251                 165                 170                 175
254 His Ile Lys Gln Asp Glu Arg Val Ser Met Gly Gln Asn Gly Asp Leu
255             180                 185                 190
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262 Asn Ala His Phe Pro Gly Thr Arg Thr Ile Ile Gln Lys Glu Pro Ile
263     210                 215                 220
266 Asp Leu Arg Val Lys Pro Thr Asn Ser Met Ile Asp Arg Lys Pro Arg
267 225                 230                 235                 240
270 Leu Leu Phe Pro Thr Asn Ser Ser Ser His Leu Val Ala Leu Gln Gly
271                 245                 250                 255
274 Gln Ser Leu Ile Leu Glu Cys Ile Ala Glu Gly Phe Pro Thr Pro Thr
275             260                 265                 270
278 Ile Lys Trp Leu His Pro Ser Asp Pro Met Pro Thr Asp Arg Val Ile
279         275                 280                 285
282 Tyr Gln Asn His Asn Lys Thr Leu Gln Leu Leu Asn Val Gly Glu Glu
283     290                 295                 300
286 Asp Asp Gly Glu Tyr Thr Cys Leu Ala Glu Asn Ser Leu Gly Ser Ala
287 305                 310                 315                 320
290 Arg His Ala Tyr Tyr Val Thr Val Glu Ala Ala Pro Tyr Trp Leu Gln
291                 325                 330                 335
294 Lys Pro Gln Ser His Leu Tyr Gly Pro Gly Glu Thr Ala Arg Leu Asp
295             340                 345                 350
298 Cys Gln Val Gln Gly Arg Pro Gln Pro Glu Val Thr Trp Arg Ile Asn
299         355                 360                 365
302 Gly Met Ser Ile Glu Lys Val Asn Lys Asp Gln Lys Tyr Arg Ile Glu
303     370                 375                 380
306 Gln Gly Ser Leu Ile Leu Ser Asn Val Gln Pro Ser Asp Thr Met Val
307 385                 390                 395                 400
310 Thr Gln Cys Glu Ala Arg Asn Gln His Gly Leu Leu Leu Ala Asn Ala
311                 405                 410                 415
314 Tyr Ile Tyr Val Val Gln Leu Pro Ala Arg Ile Leu Thr Lys Asp Asn
315             420                 425                 430
318 Gln Thr Tyr Met Ala Val Glu Gly Ser Thr Ala Tyr Leu Leu Cys Lys
319         435                 440                 445
322 Ala Phe Gly Ala Pro Val Pro Ser Val Gln Trp Leu Asp Glu Glu Gly
323     450                 455                 460
326 Thr Thr Val Leu Gln Asp Glu Arg Phe Phe Pro Tyr Ala Asn Gly Thr
327 465                 470                 475                 480
330 Leu Gly Ile Arg Asp Leu Gln Ala Asn Asp Thr Gly Arg Tyr Phe Cys
331                 485                 490                 495
334 Gln Ala Ala Asn Asp Gln Asn Asn Val Thr Ile Leu Ala Asn Leu Gln
335             500                 505                 510
338 Val Lys Glu Ala Thr Gln Ile Thr Gln Gly Pro Arg Ser Thr Ile Glu
339         515                 520                 525
342 Lys Lys Gly Ala Arg Val Thr Phe Thr Cys Gln Ala Ser Phe Asp Pro
343     530                 535                 540
346 Ser Leu Gln Ala Ser Ile Thr Trp Arg Gly Asp Gly Arg Asp Leu Gln
347 545                 550                 555                 560
350 Glu Arg Gly Asp Ser Asp Lys Tyr Phe Ile Glu Asp Gly Gln Leu Val
351                 565                 570                 575
354 Ile Gln Ser Leu Asp Tyr Ser Asp Gln Gly Asn Tyr Ser Cys Val Ala
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358 Ser Thr Glu Leu Asp Glu Val Glu Ser Arg Ala Gln Leu Leu Val Val
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363     610                 615                 620
366 Leu Lys Gln Ser Gln Val His Leu Ser Trp Ser Pro Ala Glu Asp His
367 625                 630                 635                 640
370 Asn Ser Pro Ile Glu Lys Tyr Asp Ile Glu Phe Glu Asp Lys Glu Met
371                 645                 650                 655
374 Ala Pro Glu Lys Trp Phe Ser Leu Gly Lys Val Pro Gly Asn Gln Thr
375                 660                 665                 670
378 Ser Thr Thr Leu Lys Leu Ser Pro Tyr Val His Tyr Thr Phe Arg Val
379         675                 680                 685
382 Thr Ala Ile Asn Lys Tyr Gly Pro Gly Glu Pro Ser Pro Val Ser Glu
383     690                 695                 700
386 Thr Val Val Thr Pro Glu Ala Ala Pro Glu Lys Asn Pro Val Asp Val
387 705                 710                 715                 720
390 Arg Gly Glu Gly Asn Glu Thr Asn Asn Met Val Ile Thr Trp Lys Pro
391                 725                 730                 735
394 Leu Arg Trp Met Asp Trp Asn Ala Pro Gln Ile Gln Tyr Arg Val Gln
395                 740                 745                 750
398 Trp Arg Pro Leu Gly Lys Gln Glu Thr Trp Lys Glu Gln Thr Val Ser
399         755                 760                 765
402 Asp Pro Phe Leu Val Val Ser Asn Thr Ser Thr Phe Val Pro Tyr Glu
403     770                 775                 780
406 Ile Lys Val Gln Ala Val Asn Asn Gln Gly Lys Gly Pro Glu Pro Gln
407 785                 790                 795                 800
410 Val Thr Ile Gly Tyr Ser Gly Glu Asp Tyr Pro Gln Val Ser Pro Glu
411                 805                 810                 815
414 Leu Glu Asp Ile Thr Ile Phe Asn Ser Ser Thr Val Leu Val Arg Trp
415                 820                 825                 830
418 Arg Pro Val Asp Leu Ala Gln Val Lys Gly His Leu Arg Gly Tyr Asn
419         835                 840                 845
422 Val Thr Tyr Trp Trp Lys Gly Ser Gln Arg Lys His Ser Lys Arg His
423     850                 855                 860
426 Val His Lys Ser His Met Val Val Pro Ala Asn Thr Thr Ser Ala Ile
427 865                 870                 875                 880
430 Leu Ser Gly Leu Arg Pro Tyr Ser Ser Tyr His Val Glu Val Gln Ala
431                 885                 890                 895
434 Phe Asn Gly Arg Gly Leu Gly Pro Ala Ser Glu Trp Thr Phe Ser Thr
435                 900                 905                 910
438 Pro Glu Gly Val Pro Gly His Pro Glu Ala Leu His Leu Glu Cys Gln
439         915                 920                 925
442 Ser Asp Thr Ser Leu Leu Leu His Trp Gln Pro Pro Leu Ser His Asn
443     930                 935                 940
446 Gly Val Leu Thr Gly Tyr Leu Leu Ser Tyr His Pro Leu Asp Gly Glu
447 945                 950                 955                 960
450 Ser Lys Glu Gln Leu Phe Phe Asn Leu Ser Asp Pro Glu Leu Arg Thr
451                 965                 970                 975
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**VERIFICATION SUMMARY** DATE: 12/30/2005
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date